

## SEQUENCE LISTING

<110> MIYATA, Toshio

<120> A Method for Detecting Megsin Protein and Use  
Thereof

<130> F2-101DP1PCT

<140>

<141>

<150> JP 1999-75305

<151> 1999-03-19

<150> JP 1999-306623

<151> 1999-10-28

<160> 21

<170> PatentIn Ver. 2.0

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1140)

&lt;300&gt;

<302> A mesangium-predominant gene, megsin, is a new serpin  
upregulated in IgA nephropathy.

&lt;303&gt; J. Clin. Invest.

&lt;304&gt; 120

&lt;305&gt; 4

&lt;306&gt; 828-836

&lt;307&gt; 1998-08-15

&lt;400&gt; 1

atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48

Met Ala Ser Leu Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe

1

5

10

15

aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96

Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20

25

30

ctg agc ctc ttc gct gcc ctg gcc ctg gtc cgc ttg ggc gct caa gat 144

Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp

35

40

45

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca	192	
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser		
50	55	60
gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg	240	
Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu		
65	70	75
aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc	288	
Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu		
85	90	95
agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag	336	
Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys		
100	105	110
gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga	384	
Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg		
115	120	125
gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag	432	
Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys		
130	135	140
tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa	480	

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu  
 145                    150                    155                    160

ggt ggc ata agc tca tct gct gta atg gtg ctg gtg aat gct gtg tac 528  
 Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
 165                    170                    175

ttc aaa ggc aag tgg caa tca gcc ttc acc aag agc gaa acc ata aat 576  
 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn  
 180                    185                    190

tgc cat ttc aaa tct ccc aag tgc tct ggg aag gca gtc gcc atg atg 624  
 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met  
 195                    200                    205

cat cag gaa cgg aag ttc aat ttg tct gtt att gag gac cca tca atg 672  
 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met  
 210                    215                    220

aag att ctt gag ctc aga tac aat ggt ggc ata aac atg tac gtt ctg 720  
 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu  
 225                    230                    235                    240

ctg cct gag aat gac ctc tct gaa att gaa aac aaa ctg acc ttt cag 768  
 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln  
 245                    250                    255

aat cta atg gaa tgg acc aat cca agg cga atg acc acc tct aag tat gtt			816
Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val			
260	265	270	
gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa			864
Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys			
275	280	285	
caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa			912
Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys			
290	295	300	
gca gat ctc tct ggg att gct tcg ggg ggt cgt ctg tat ata tca agg			960
Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg			
305	310	315	320
atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct			1008
Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala			
325	330	335	
act gct gcc aca gga agt aat att gta gaa aag caa ctc cct cag tcc			1056
Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser			
340	345	350	
acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat			1104

Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp

355 360 365

gac atc atc tta ttc agt ggc aaa gtt tct tgc cct tga 1143

Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro

370 375 380

<210> 2

<211> 380

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe

1 5 10 15

Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20 25 30

Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp

35 40 45

Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser

50 55 60

Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu

65

70

75

80

Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu

85

90

95

Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys

100

105

110

Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg

115

120

125

Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys

130

135

140

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu

145

150

155

160

Gly Gly Ile Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr

165

170

175

Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn

180

185

190

Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met

195

200

205

His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met

210

215

220

Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu

225

230

235

240

Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln

245

250

255

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val

260

265

270

Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys

275

280

285

Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys

290

295

300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg

305

310

315

320

Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala

325

330

335

Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser

340

345

350

Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp

355

360

365

Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro

370

375

380

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized degenerative primer sequence

<220>

<221> misc\_feature

<222> 26, 29

<223> n is a or g or c or t.

<400> 3

gtgaatgctg tgtacttaaa ggcaantgn

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized degenerative primer sequence

<220>

<221> misc\_feature

<222> 3, 9, 15

<223> n is a or g or c or t.

<400> 4

aanagraang grtengc

17

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially

synthesized degenerative primer sequence

<220>

<221> misc\_feature

<222> 6, 9, 12, 15, 18, 21

<223> n is a or g or c or t.

<400> 5

atggcntcng cngcngcngc naaygc

26

<210> 6

<211> 37

<212> DNA

## <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially

synthesized degenerative primer sequence

<400> 6

cgacctccag aggcaattcc agagagatca gccctgg

37

<210> 7

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized degenerative primer sequence

<400> 7

gtcttccaag cctacagatt tcaagtggct cctc

34

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized antisense primer sequence

<400> 8

gctcaggca gtgaagatgc tcagggaga

30

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized antisense primer sequence

<400> 9

ctgacgtgca cagtcacctc gagcacc

27

<210> 10

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized sense primer sequence

<400> 10

gaggtctcag aagaaggcac tgaggcaact gctgcc

36

<210> 11

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

<400> 11

Phe Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe  
1 5 10 15

<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

<400> 12

Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val Phe Ser Asp  
1 5 10 15

<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

<400> 13

Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu

1

5

10

15

<210> 14

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

<400> 14

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val

1

5

10

15

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

<400> 15

Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu Phe Arg

1

5

10

15

<210> 16

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

<400> 16

Leu Gly Leu Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp

1

5

10

&lt;210&gt; 17

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:Artificially  
synthesized domain peptide of human megsin

&lt;400&gt; 17

Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser Thr Val

1

5

10

&lt;210&gt; 18

&lt;211&gt; 1229

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (8)..(1147)

&lt;220&gt;

<221> misc\_feature

<222> 158, 159, 160, 287, 288, 289

<223> n is a or g or c or t.

<300>

<310> PCT/JP98/04269

<311> 1998-09-22

<400> 18

tttcaaa atg gcc tcc ctt gct gca gca aat gca gaa ttt ggc ttc gac	49	
Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp		
1	5	10

tta ttc aga gag atg gat agt agt caa gga aac gga aat gta ttc ttc	97		
Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe			
15	20	25	30

tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct	145	
Ser Ser Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala		
35	40	45

cga ggt gac tgt nnn cgt cag att gac aag gcc ctg cac ttt atc tcc	193	
Arg Gly Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser		
50	55	60

cca tca aga caa ggg aat tca tcg aac agt cag cta gga ctg caa tat	241
---	-----

Pro Ser Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr

65                   70                   75

caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag gat nnn   289

Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa

80                   85                   90

aaa ctc agc att gcc aat gga gtt ttt gca gag aaa gta ttt gat ttt   337

Lys Leu Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe

95                   100                  105                  110

cat aag agc tat atg gag tgt gct gaa aac tta tac aat gct aaa gtg   385

His Lys Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val

115                  120                  125

gaa aga gtt gat ttt aca aat gat ata caa gaa acc aga ttt aaa att   433

Glu Arg Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile

130                  135                  140

aat aaa tgg att gaa aat gaa aca cat ggc aaa atc aag aag gtg ttg   481

Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu

145                  150                  155

ggg gac agc agc ctc agc tca tca gct gtc atg gtg cta gtg aat gct   529

Gly Asp Ser Ser Leu Ser Ser Ala Val Met Val Leu Val Asn Ala

160                  165                  170

gtt tac ttc aaa ggc aag tgg aaa tcg gcc ttc acc aag agt gat acc 577

Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr

175

180

185

190

ctc agt tgc cat ttc agg tct ccc agc ggt cct gga aaa gca gtt aat 625

Leu Ser Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn

195

200

205

atg atg cat caa gaa cgg agg ttc aat ttg tct acc att cag gag cca 673

Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro

210

215

220

cca atg cag att ctt gag cta caa tat cat ggt ggc ata agc atg tac 721

Pro Met Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr

225

230

235

atc atg ttg ccc gag gat gac cta tcc gaa att gaa agc aag ctg agt 769

Ile Met Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser

240

245

250

ttc cag aat cta atg gac tgg aca aat agc agg aag atg aaa tct cag 817

Phe Gln Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln

255

260

265

270

tat gtg aat gtg ttt ctc ccc cag ttc aag ata gag aaa gat tat gaa 865

Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu

275

280

285

atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag 913

Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu

290

295

300

tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta 961

Ser Arg Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val

305

310

315

tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc 1009

Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr

320

325

330

gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct 1057

Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro

335

340

345

350

gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg 1105

Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg

355

360

365

aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct 1147

Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

370

375

380

tgaaattcta tttggtttcc catacactaa caggcatgaa gaaacatcat aagtgaatag 1207

aattgttaatt ggaagtacat gg 1229

<210> 19

<211> 380

<212> PRT

<213> Rattus norvegicus

<220>

<221> misc\_feature

<222> 51, 94

<223> Xaa is unknown.

<400> 19

Met Ala Ser Leu Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe

1

5

10

15

Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser

20

25

30

Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly

35

40

45

Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser

50 55 60

Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu

65 70 75 80

Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu

85 90 95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys

100 105 110

Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg

115 120 125

Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys

130 135 140

Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp

145 150 155 160

Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr

165 170 175

Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser

180 185 190

Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met

195 200 205

His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met

210 215 220

Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met

225 230 235 240

Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln

245 250 255

Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val

260 265 270

Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg

275 280 285

Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg

290 295 300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys

305 310 315 320

Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala

325

330

335

Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser

340

345

350

Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn

355

360

365

Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

370

375

380

&lt;210&gt; 20

&lt;211&gt; 1147

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1104)

&lt;300&gt;

&lt;310&gt; PCT/JP98/04269

&lt;311&gt; 1998-09-22

&lt;400&gt; 20

ttc gac tta ttc aga gag atg gat agt agc caa gga aat gga aat gta 48  
 Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val

1 5 10 15

ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg 96  
 Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu  
 20 25 30

ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt 144  
 Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe  
 35 40 45

aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt 192  
 Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu  
 50 55 60

cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag 240  
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys  
 65 70 75 80

gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat 288  
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr  
 85 90 95

gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct 336  
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala

100

105

110

aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt 384  
 Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe

115

120

125

aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag 432  
 Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys

130

135

140

gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg 480  
 Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val  
 145 150 155 160

aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act 528  
 Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr

165

170

175

gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta 576  
 Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val  
 180 185 190

gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag 624  
 Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln

195

200

205

cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc			672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser			
210	215	220	
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag			720
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys			
225	230	235	240
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa			768
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys			
245	250	255	
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat			816
Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn			
260	265	270	
tat gaa atg acg cac cac ttg aaa tcc tta ggc ttg aaa gat atc ttt			864
Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe			
275	280	285	
gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc			912
Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu			
290	295	300	
tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag			960
Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu			

305

310

315

320

ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag 1008  
 Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln

325

330

335

ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc 1056  
 Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val

340

345

350

atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct 1104  
 Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

355

360

365

tgaaattcga ttgggttcc tatacagtaa caggcatcaa gaa 1147

&lt;210&gt; 21

&lt;211&gt; 368

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 21

Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val

1

5

10

15

Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu

20 25 30

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe

35 40 45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu

50 55 60

Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys

65 70 75 80

Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr

85 90 95

Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala

100 105 110

Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe

115 120 125

Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys

130 135 140

Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val

145 150 155 160

Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr

165 170 175

Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val

180 185 190

Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln

195 200 205

Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser

210 215 220

Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys

225 230 235 240

Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys

245 250 255

Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn

260 265 270

Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe

275 280 285

Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu

290

295

300

Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu

305

310

315

320

Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln

325

330

335

Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val

340

345

350

Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

355

360

365